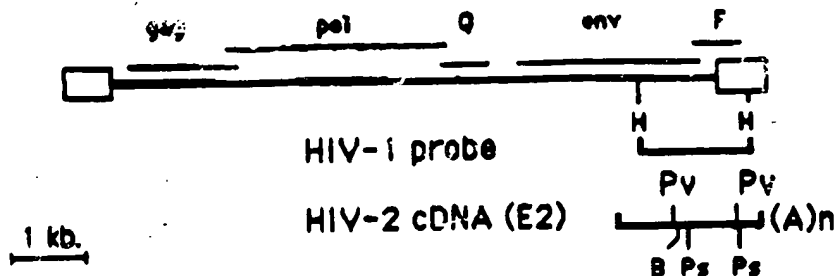


79

A



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B

Diagram illustrating the sequence alignment of HIV-2 and HIV-1 cDNA (E2) regions. The sequences are aligned, showing gaps (---) and specific nucleotide positions (9000, 9010, 9020, 9030, 9040, 9050, 9060, 9070, 9080, 9090, 9100, 9110, 9120, 9130, 9140, 9150, 9160, 9170, 9180, 9190, 9200, 9210, 9220). Restriction sites Pvu II and Pst I are indicated. A boxed region highlights a specific sequence motif. The alignment is labeled U3/R and R.

HIV-2: AGTAACTAACAGAA-----ACAGCTGAGACTGC-----AGGGACTTTCAGAAAGGGGCTG
 HIV-1: AGT-ACCTTCAAGAACTGCTGACATC-GAGCTTGCTACAAGGGACTTTCGGCTGGGGACTT
 9000 9010 9020 9030 9040

HIV-2: TAACGAA-----GGGAGGGACATGGGAG-----GAGCTGGTGGGGAACGCCTC
 HIV-1: T-CCAGGGAGGGCGTGGCCTGGGCCGGGACTGGGGAGTGGCGAGC-----CCTC
 9050 9060 9070 9080 9090

HIV-2: AATTTCTGTGATAAAATATACCCGCTGCTTGCAATTGTACTTCAGTGGCTCTGCGGAGAGG
 HIV-1: AGATG--CTGCATATAAGCAGCTGCTTTTTGCC-TGTACTGG-GTCTCTCTGGTTAGAC-
 9100 9110 9120 9130 9140

HIV-2: CTGGGAGATTGAGCCCTGGGAGCTTCTCTCCAGCACTAGCAGGTAGAGCCCTGGGTCTCCC
 HIV-1: ---CAGATTGAGCCTGGGAGC-TCTCTGGCTAACTAGGGAACCCAC-----
 9150 9160 9170 9180 9190

HIV-2: TGCTAGACTCTCACCAGCACTTGGCCGGTGCTGGGCAGACGGCCCCACGCTTGCTTGCTT
 HIV-1: -----TGCTT

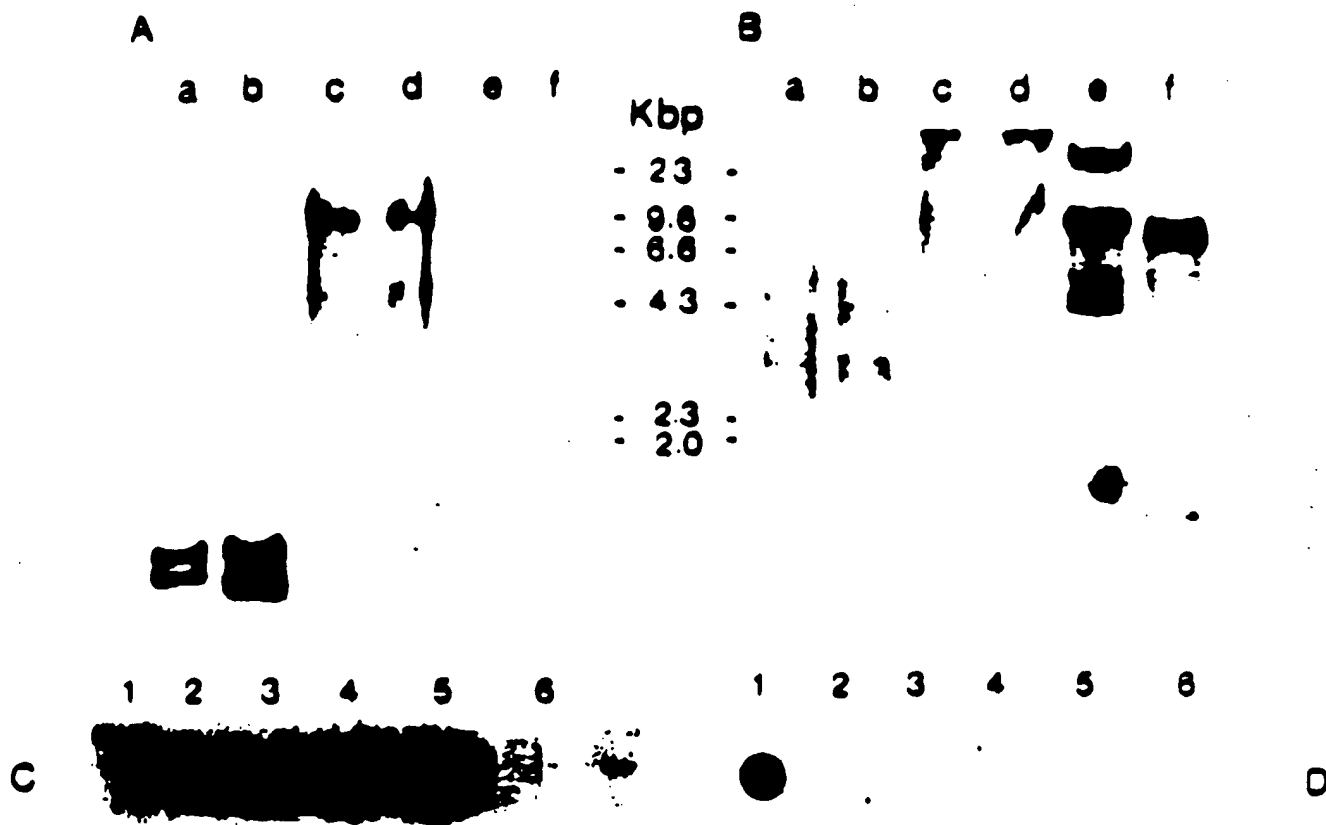
HIV-2: AAAAACCTCCTTAATAAAGCT-GCC---AGTAGAAGCA
 HIV-1: AAG-----CCTCAATAAAGCTTGCCTTGAGTGCTTCAA
 9210 9220

Restriction sites: Pvu II, Pst I, Hind III.

Labels: U3/R, R.

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SCANNED # 70

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Fig. 3

HIV-2 probe

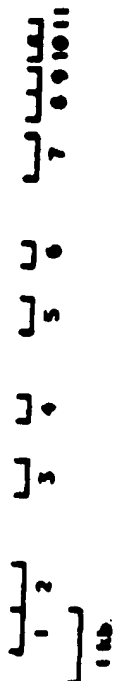
	1	2	3	4	5	6	7	8	9	10	11	12
En-42
En-20
En-3

ROD 27

ROD 35

HIV-1 probe

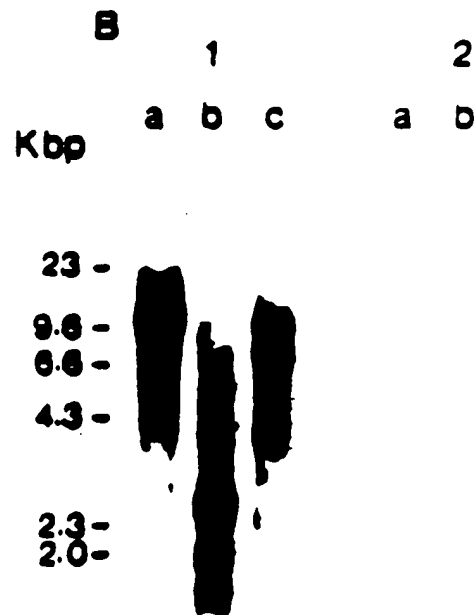
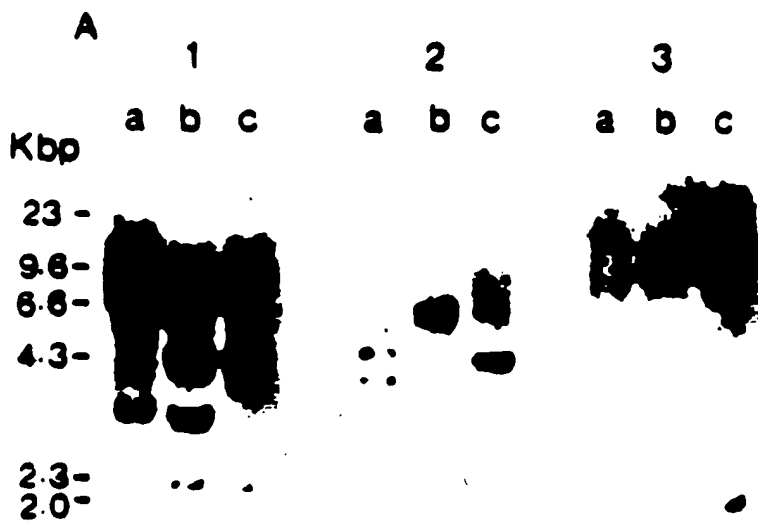
En-3
------	---	---	---	---	---	---	---	---	---	---	---	---



ROD 4

ROD 4

Fig. 4



HIV-2 RNA

$$3\sigma_H(A) \leq R_1 \leq U_3$$


No sites in pSfE2 insert for: AccI/AvaI/BclI/BspI/ClaI/EcoRI/HhaI/HindIII/KpnI/NdeI/NruI/PvuI/SacI/SmaI/XbaI

FIG. 1A

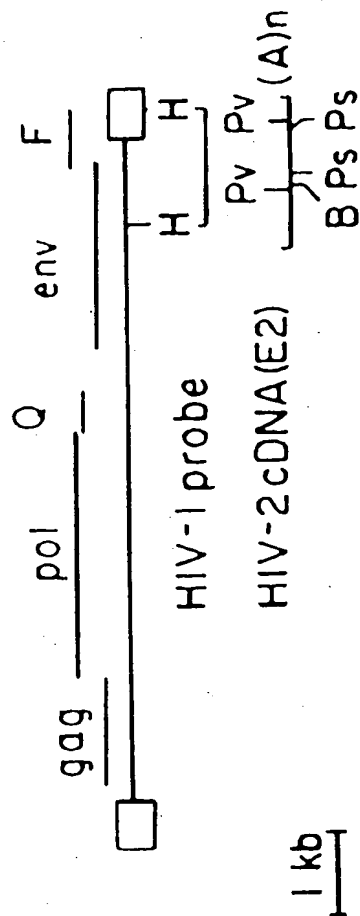


FIG. 1B

		PvuI	PstI
HIV.2	AGTA ¹ ACTAACAGAA-----ACAGCTGAGACTGC---AGGGACTTCCAGAGGGGCTG		
HIV.1	AGT- ¹ ACTTCAAGAACTGCTGACATC- ¹ GAGCTT ¹ GCTACAAAGGGACTTCCGCTGGGGACTT	9010 9020 9030 9040	
HIV.2	TAACCAA-----GGGAGGGACATGGGAG---GAGCTGGTGGGGAACGCCCTC		
HIV.1	T---CCAGGGAGGCGTGGCCTGGCGGGGACTGGGGAGTGGCGAGC-----CCTC	9050 9060 9070 9080 9090	
HIV.2	ATATTCTCTGTATAAATATACCCGCTGCTTGCAATTGACTTCAGTCGCTCTGCGGAGAGG		
HIV.1	AGATG--CTGCA ¹ ATAAGCAGCTGCTTTTGGCC-TGTACTGG-GTCTCTCTGTTAGAC-	9100 9110 9120 9130 9140	
HIV.2	CTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAGAGCCTGGGTGTCCTC		
HIV.1	----CAGATT ¹ TGAGCCTGGGAGC-TCTCTGGCTAACTAGGGAACCCAC-----	9150 9160 9170 9180 9190	
HIV.2	TGCTAGACTCTCACCAGCACTTGGCCGGTGCTGGGCAGACGGCCCCACGCTTGCTTGCTT		
HIV.1	-----TGCTT		
HIV.2	AAAAACCTCCTTAA ¹ TAAAGCT-GCC---AGTAGAAGCA		
HIV.1	AAG-----CCTCA ¹ ATAAGCTTGCCTTGAGGTGCTTCAA	9210 9220	
		Hind III	R

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FIG. 2A

FIG. 2A

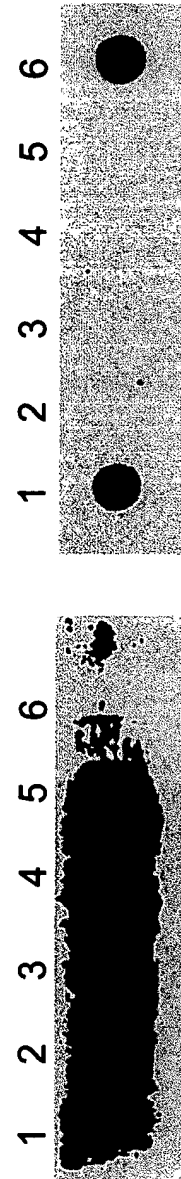
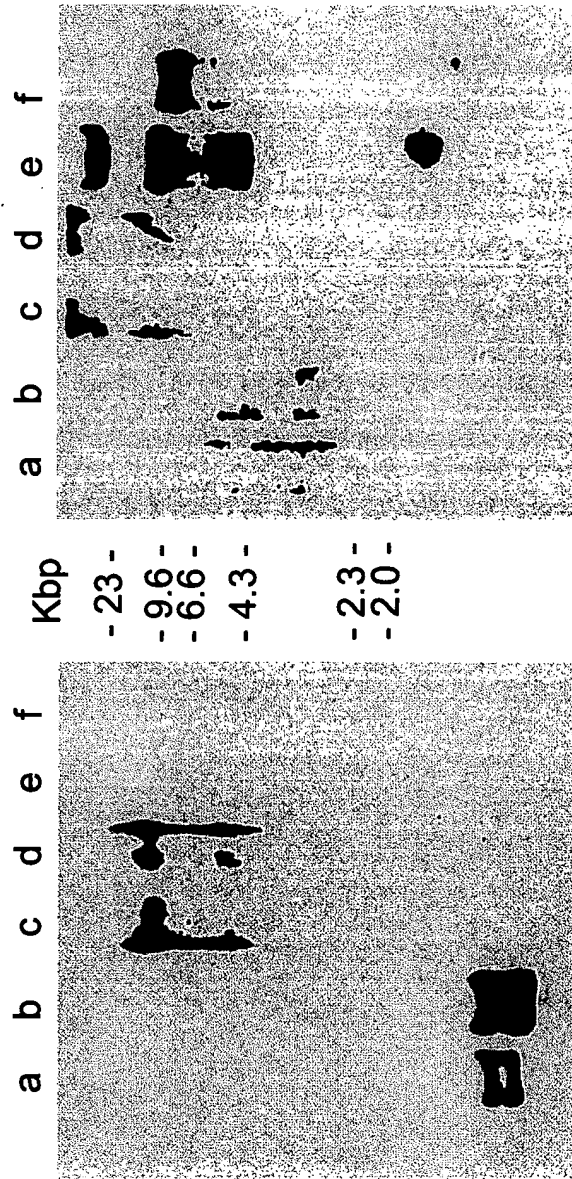
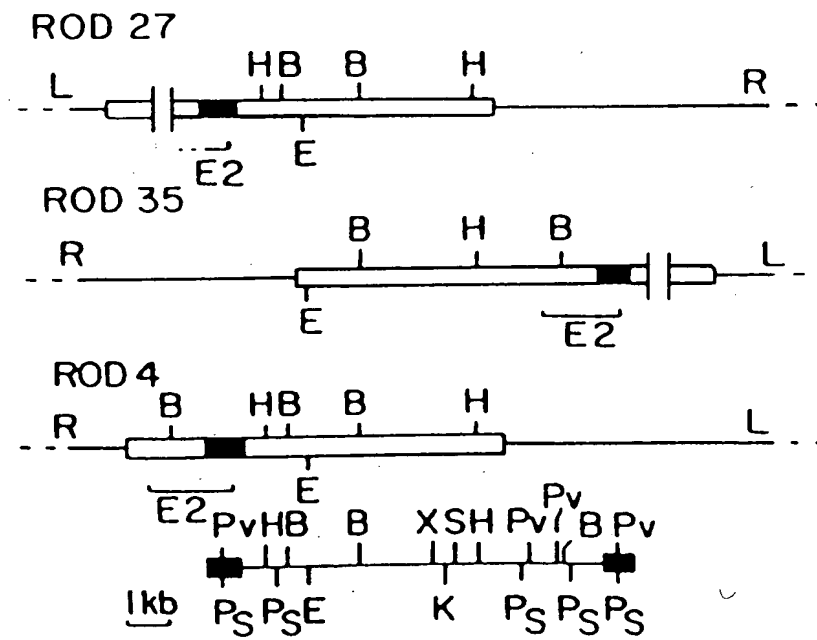


FIG. 2C

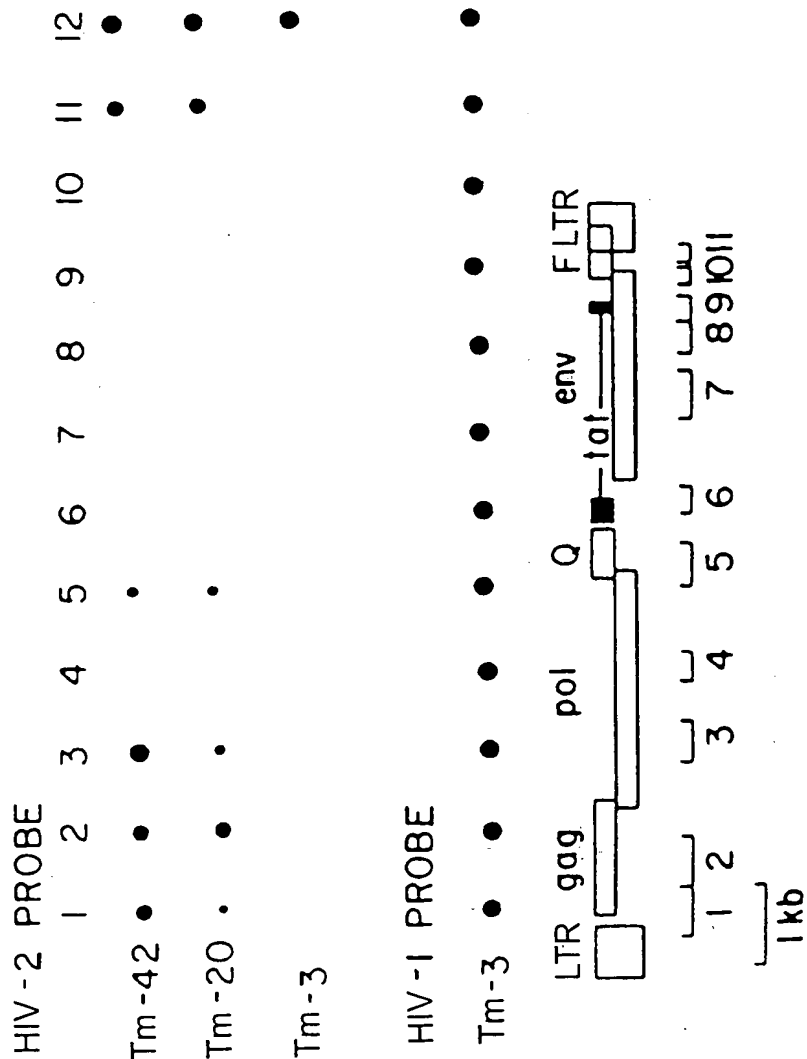
FIG. 2D

FIG. 3A



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FIG. 3B



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FIG. 4B

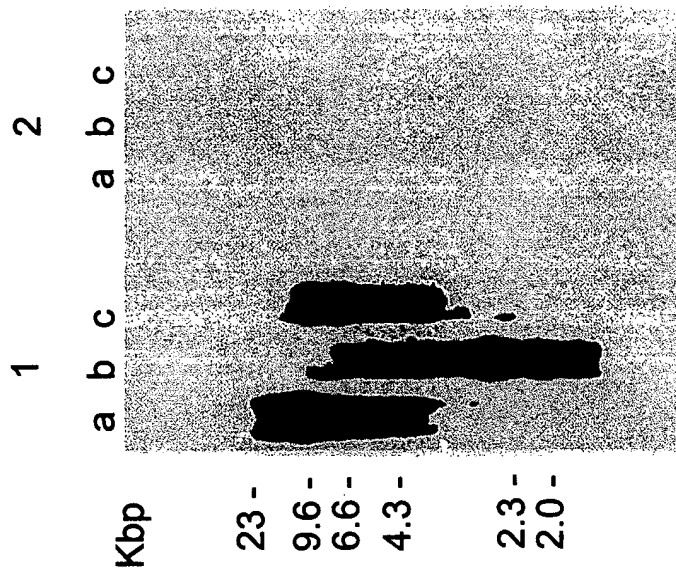


FIG. 4A

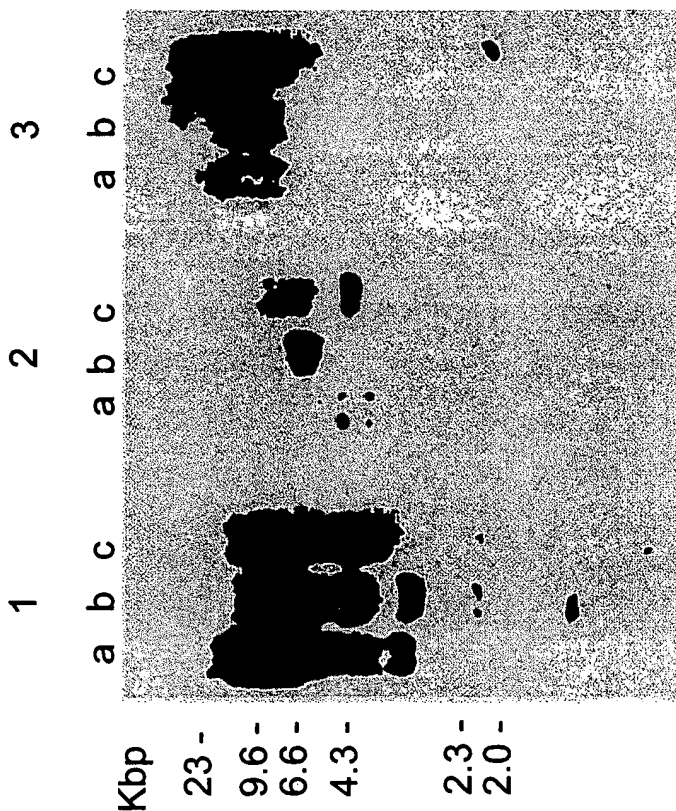
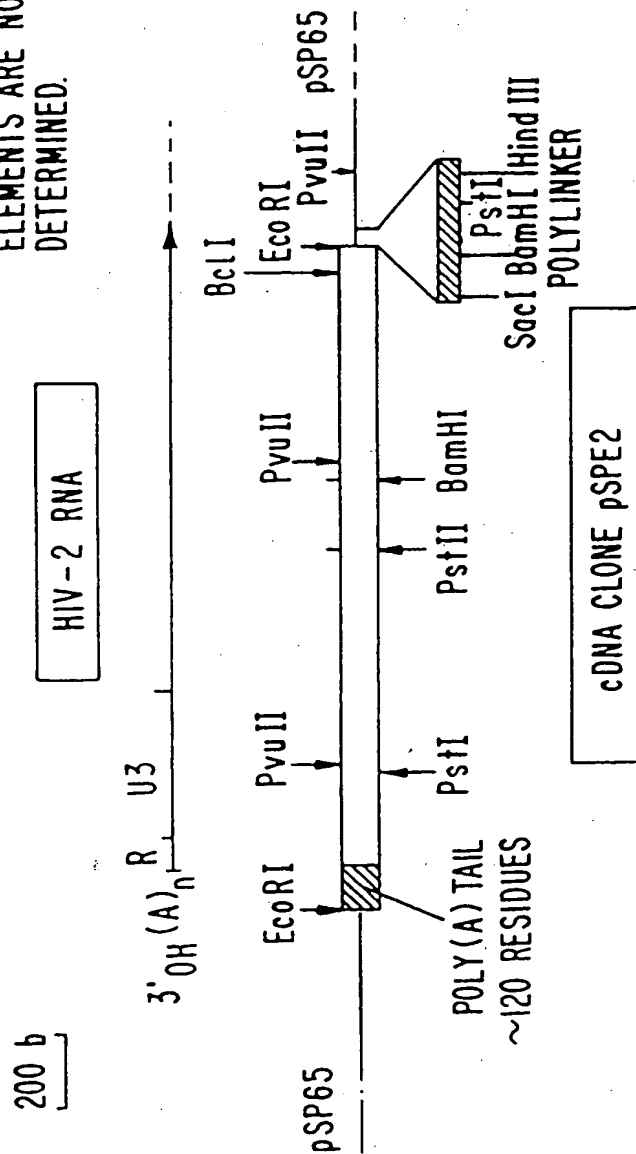


FIG. 5

THE BOUNDARIES OF R AND U3
ELEMENTS ARE NOT PRECISELY
DETERMINED.



NO SITES IN pSPE2 INSERT FOR: AccI/AvaI/BclI/BglII/ClaI/EcoRI

HincII/HindIII/KpnI/NdeI/NruI/PvuI/

SacI/SmaI/SalI/XbaI